```
=> d his

     (FILE 'HOME' ENTERED AT 15:13:01 ON 12 JAN 2006)

     FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 15:13:45 ON 12 JAN
     2006
L1         24946 S STOP CODON OR STOP SIGNAL
L2           228 S L1 AND TRANSPOSON
L3             5 S L2 AND END SEQUENCE
L4           125 S (MODIFY OR CHANGE OR ALTER OR MUTATE OR TRUNCATE) AND END SEQ
L5             2 S L4 AND L1
L6             1 DUP REMOVE L5 (1 DUPLICATE REMOVED)
L7             9 S L4 AND TRANSPOSON
L8             3 DUP REMOVE L7 (6 DUPLICATES REMOVED)

=>
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 NEWS  5  DEC 14   2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
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 NEWS  7  DEC 21   IPC search and display fields enhanced in CA/CAplus with the
                   IPC reform
 NEWS  8  DEC 23   New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
                   USPAT2

 NEWS EXPRESS  JANUARY 03 CURRENT VERSION FOR WINDOWS IS V8.01,
               CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
               V8.0 USERS CAN OBTAIN THE UPGRADE TO V8.01 AT
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FILE 'SCISEARCH' ENTERED AT 15:13:45 ON 12 JAN 2006
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```
=> s stop codon or stop signal
L1       24946 STOP CODON OR STOP SIGNAL

=> s l1 and transposon
L2         228 L1 AND TRANSPOSON

=> s l2 and end sequence
   2 FILES SEARCHED...
L3           5 L2 AND END SEQUENCE

=>

=> d ibib abs 1-5

L3   ANSWER 1 OF 5     MEDLINE on STN
ACCESSION NUMBER:   2003372847     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 12907724
TITLE:              The bacterial transposon Tn7 causes premature
                    polyadenylation of mRNA in eukaryotic organisms: TAGKO
                    mutagenesis in filamentous fungi.
AUTHOR:             Lo Clive; Adachi Kiichi; Shuster Jeffrey R; Hamer John E;
                    Hamer Lisbeth
CORPORATE SOURCE:   Paradigm Genetics, Inc., 108 Alexander Drive, Research
                    Triangle Park, NC 27709, USA.. clivelo@hkucc.hku.hk
SOURCE:             Nucleic acids research, (2003 Aug 15) 31 (16) 4822-7.
                    Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY:       England: United Kingdom
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200401
ENTRY DATE:         Entered STN: 20030809
                    Last Updated on STN: 20040130
                    Entered Medline: 20040129
AB   TAGKO is a Tn7-based transposition system for genome wide mutagenesis in
     filamentous fungi. The effects of transposon insertion on the
     expression of TAGKO alleles were examined in Magnaporthe grisea and
     Mycosphaerella graminicola. Northern analysis showed that stable,
     truncated transcripts were expressed in the TAGKO mutants. Mapping of the
     3'-ends of TAGKO cDNAs revealed that they all contain Tn7 end
     sequences, regardless of the transposon orientation.
     Polyadenylation signals characteristic of eukaryotic genes, preceded by
     stop codons in all frames, are located in both ends of
     the bacterial transposon. Thus, TAGKO transcripts are
     prematurely polyadenylated, and truncated proteins are predicted to be
     translated in the fungal mutants. Depending on the extent of protein
     truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate
     dioxygenase) resulted in tyrosine sensitivity in the two fungi.
     Similarly, a particular M.grisea CBS1 (encoding cystathionine
     beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a
     yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo
     study of truncated gene products in filamentous fungi.

L3   ANSWER 2 OF 5  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:        2003:837288  CAPLUS
DOCUMENT NUMBER:         139:333968
TITLE:                   Producing deletion derivatives of polypeptides using
                         modified transposon with stop
                         codons in all three reading frames
INVENTOR(S):             Savilahti, Harri; Tieaho, Ville
PATENT ASSIGNEE(S):      Finnzymes Oy, Finland
SOURCE:                  PCT Int. Appl., 37 pp.
                         CODEN: PIXXD2
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  1
PATENT INFORMATION:
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PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003087370	A1	20031023	WO 2003-FI285	20030414
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
FI 2002000746	A	20031019	FI 2002-746	20020418
US 2005208616	A1	20050922	US 2005-511327	20050330
PRIORITY APPLN. INFO.:			FI 2002-746 A	20020418
			WO 2003-FI285 W	20030414

AB The present invention describes an in vitro transposition-based methodol. for generation of deletion derivs. of polypeptides. An artificial **transposon** containing at least partly within its **transposon** ends a modification with translation **stop codons** in three reading frames is provided. In the method, transposition complexes are assembled using the modified **transposon** and essentially random integrations into the target plasmid, containing a polypeptide coding nucleic acid of interest, are recovered as a plasmid pool. Subsequent manipulation steps including restriction enzyme digestions and ligation result in pools of mutant clones from which deletion derivs. of a polypeptide coding nucleic acid of interest and its resp. deletion polypeptides could be produced.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:616864 CAPLUS

DOCUMENT NUMBER: 139:318350

TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi

AUTHOR(S): Lo, Clive; Adachi, Kiichi; Shuster, Jeffrey R.; Hamer, John E.; Hamer, Lisbeth

CORPORATE SOURCE: Paradigm Genetics, Inc., Research Triangle Park, NC, 27709, USA

SOURCE: Nucleic Acids Research (2003), 31(16), 4822-4827
CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern anal. showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular M.grisea CBS1 (encoding cystathionine β-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 5 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:563096 BIOSIS
DOCUMENT NUMBER: PREV200300564228
TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi.
AUTHOR(S): Lo, Clive [Reprint Author]; Adachi, Kiichi; Shuster, Jeffrey R.; Hamer, John E.; Hamer, Lisbeth
CORPORATE SOURCE: Department of Botany, The University of Hong Kong, Pokfulam Road, Hong Kong, China
clivelo@hkucc.hku.hk
SOURCE: Nucleic Acids Research, (August 15 2003) Vol. 31, No. 16, pp. 4822-4827. print.
ISSN: 0305-1048 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Dec 2003
Last Updated on STN: 3 Dec 2003

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern analysis showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular M. grisea CBS1 (encoding cystathionine beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.

L3 ANSWER 5 OF 5 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:724714 SCISEARCH
THE GENUINE ARTICLE: 712DY
TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi
AUTHOR: Lo C (Reprint); Adachi K; Shuster J R; Hamer J E; Hamer L
CORPORATE SOURCE: Univ Hong Kong, Dept Bot, Pokfulam Rd, Hong Kong, Hong Kong, Peoples R China (Reprint); Univ Hong Kong, Dept Bot, Hong Kong, Hong Kong, Peoples R China; Paradigm Genet Inc, Res Triangle Pk, NC 27709 USA
COUNTRY OF AUTHOR: Peoples R China; USA
SOURCE: NUCLEIC ACIDS RESEARCH, (15 AUG 2003) Vol. 31, No. 16, pp. 4822-4827.
ISSN: 0305-1048.
PUBLISHER: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 33
ENTRY DATE: Entered STN: 5 Sep 2003
Last Updated on STN: 5 Sep 2003
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in Magnaporthe grisea and Mycosphaerella graminicola. Northern analysis showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by

stop codons in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular M.grisea CBS1 (encoding cystathionine beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.